Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88

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Supplementary Table 5 Genes implicated in asexual and sexual reproduction in *A. niger*

Gene[1]	Function	*A. niger*	*A. nidulans*	*A. fumigatus*	*A. oryzae*
Signal Transduction - Asexual Reproduction					
fluG	Similarity to glutamine synthetase; signalling molecule	An14g03390	AN4819.2	Afu3g07140	AO090020000217
gprD	Receptor prevents improper sexual development	An02g01560	AN3387.2	Afu2g12640	AO090026000360
fphA	Red light phytochrome	An14g02970	AN9008.2	89.m01927	AO070336000118
fadA (GPA1)	Alpha-subunit G protein	An08g06130	AN0651.2	Afu1g13140	AO090012000577
GanB	Alpha-subunit G protein	An08g05820	AN1016.2	Afu1g12930	AO090012000600
sfaD (STE 4)	Beta-subunit G protein	An18g02090	AN0081.2	Afu5g12210	AO090120000339
flbA	Regulator of G-protein signalling	An02g03160	AN5893.2	Afu2g11180	AO090026000532
rgsA	Regulator of G-protein signalling	An18g06110	AN5755.2	Afu6g06860	AO090003000066
flbC	Putative regulator containing two zinc-fingers	An02g05420	AN2421.2	Afu2g13770	AO090026000200
flbD	strong similarity to myb-like DNA binding protein	An01g04830	AN0279.2	Afu1g03210	AO090005000765
sakA	MAP kinase represses sexual development	An08g05850	AN1017.2	70.m15235	AO070343000598
steC (STE11)	Serine/threonine protein kinase MKKK	An17g01280	AN2269.2	Afu5g06420	AO090009000610
cyaA	adenylate cyclase	An11g01520	AN3913.2	Afu6g08520	AO090001000512
pkaR	protein kinase A regulatory subunit	An16g03740	AN4987.2	Afu3g10000	AO090003000534
rasA	RAS protein *A. fumigatus*	An01g02320	AN0182.2	Afu5g11230	AO090026000726
rasB	RAS protein *A. fumigatus*	An05g00370	AN5832.2	Afu2g07770	AO090011000918
Conidiophore Development					
brlA	Zn (II) finger transcription factor (transition stalk to vesicle)	An01g10540	AN0973.2	Afu1g16590	AO090005001041
abaA /tec1	ATTS/TEA DNA binding domain transcription regulator	An01g03750	AN0422.2	Afu1g04830	AO090166000101
stuA /phd1	APSES-transcription factor (spatial expression of abaA)	An05g00480	AN5836.2	Afu2g07900	AO090011000905
wetA	Probable regulator of spore maturation	An01g08900	AN1937.2	Afu4g13230	AO090009000260
medA	Transcription factor	An02g02150[2]	AN6230.2	Afu2g13260	AO090026000285
dopA	Leucine zipper-like domain regulator (initiation conidiogenesis)	An11g04750	AN2094.2	Afu2g05020	AO090003000304
devR	bHLH transcription factor (phialide development)	An15g03490	AN7552.2	Afu2g14800	AO090026000797
hymA /hym1	Cell cycle regulation and polarity	An02g08420	AN3095.2	Afu3g12480	AO090005000720
apsA	Microtuble-cortex interaction (nuclear migration into metulae)	An15g02740	AN7757.2	Afu5g07710	AO090701000677
apsB	Spindle pole associated protein (nuclear migration into metulae)	An06g01620	AN3724.2	Afu6g12460	AO090009000166
csnD	Signalosome subunit 4 (regulation of conidiophore number)	An16g07210	AN1539.2	Afu8g05500	AO090005000595
csnE	Signalosome subunit 5 (regulation of conidiophore number)	An15g06660	AN2129.2	Afu2g16250	AO090102000238
phiA	Strong similarity to hypothetical cell wall protein binB	An14g01820	AN8333.2	Afu3g03060	AO090003001484
rodA	Hydrophobin (spore coat)	An04g08500	AN8803.2	Afu5g09580	AO090020000588
dewA	Hydrophobin (spore coat)	An03g02400	AN8006.2	No definite match	AO090701000610
yA	Laccase (pigment biosynthesis)	An01g13660	AN0878.2	Afu1g15670	AO090005001177
wA	Polyketide synthase (pigment biosynthesis)	An12g02050	AN0523.2	Afu3g02570	AO090010000114
ppoA	Fatty acid oxygenase for Psi factor production	An04g05880	AN1967.2	Afu4g10770	AO090003001138
ppoB	Fatty acid oxygenase for Psi factor production	No definite match	AN6320.2	No definite match	AO070319000035
ppoC	Fatty acid oxygenase for Psi factor production	An02g07930	AN5028.2	Afu3g12120	AO090003000772
Gz ppoD	Fatty acid oxygenase	An12g01320	No definite match	No definite match	AO070303000046

Mating Processes					
MAT-1 (MAT-alpha1)	Mating-type (alpha-box domain transcriptional activator)	An11g10180	AN2755.2	Not found	20164.m00251
MAT-2	Mating-type (HMG-box transcriptional activator)	Not found	AN4734.2	59.m09249	Not found
ppgA (MFalpha 1 & 2)	Pheromone precursor (alpha-factor like)	An18g06770	AN5791.2	69.m14805	20086.m00080
ppgB (MF**a**1, MF**a**2)	Pheromone precursor (**a**-factor like)	Ambiguous	Ambiguous	Not found	Not found
(KEX1)	Carboxypeptidase alpha-factor processing	An08g00430	AN1384.2	70.m14837	20080.m00038
kexB (KEX2)	Endoprotease for alpha-factor processing	An01g08530	AN3583.2	58.m07381	20179.m00626
(STE13)	Dipeptidyl aminopeptidase for alpha-factor processing	An02g11420	AN2946.2	59.m09093	20174.m00466
(STE23)	Dipeptidyl aminopeptidase for **a**-factor processing	An16g01860	AN8044.2	53.m03900	20129.m00210
(RCE1)	CAAX prenyl protease **a**-factor C-terminal processing	An14g03420	AN6528.2	62.m03116	20107.m00091
(STE24)	CAAX prenyl protease **a**-factor C and N-terminal processing	An04g01950	Yes[3]	58.m07859	20142.m00264
(RAM1/STE16)	CAAX-farnesyltransferase beta subunit; **a**-factor modification	An04g06620	AN2002.2	58.m07610	20138.m00208
(RAM2)	CAAX-farnesyltransferase alpha subunit; **a**-factor modification	An04g02210	AN3867.2	58.m07839	20142.m00239
(STE14)	CAAX-prenyl cysteine carboxymethyltransferase; **a**-factor modification	An12g03660	AN6162.2	72.m19009	20177.m00422
atrD (STE6)	ATP-dependent efflux pump for **a**-factor like pheromone	An04g03690	AN2300.2	58.m08958	20136.m00137
Signal Transduction - Sexual Reproduction					
preB/gprA (STE 2)	Pheromone Receptor (for alpha-factor like pheromone)	An09g04180	AN2520.2	59.m08468	20123.m00180
preA/gprB (STE 3)	Pheromone Receptor (for **a**-factor like pheromone)	An03g03890	AN7743.2	71.m15771	20162.m00356
gprD	Receptor prevents improper sexual development	An02g01560	AN3387.2	72.m19372	20141.m00118
fadA (GPA1)	Alpha-subunit G protein	An08g06130	AN0651.2	70.m15256	20180.m01174
sfaD (STE 4)	Beta-subunit G protein	An18g02090	AN0081.2	71.m15359	20148.m00279
gpgA (STE18)	Gamma-subunit G protein	Partial sequence[2,3]	AN2742.2	54.m06689	20175.m00541
(STE20)	Serine/threonine protein kinase MKKKK	An11g04320	AN2067.2	57.m05766	20178.m00629
steC (STE11)	Serine/threonine protein kinase MKKK	An17g01280	AN2269.2	71.m15914	20132.m00123
STE7	Serine/threonine protein kinase MKK	An11g10690	AN3422.2	59.m09275	20164.m00222
mpkB (FUS3)	Mitogen-activated protein kinase MK	An08g10670	AN3719.2	69.m15727	20178.m00764
steA (STE12)	Transcriptional Activator. Homeodomain DNA binding	An17g01580	AN2290.2	71.m15938	20132.m00151
(STE50)	Pheromone adaptation feedback response	An04g09220	AN7252.2	72.m19797	20134.m00115
Nc ham-2 (FAR11)	Transmembrane protein required for mating cell fusion	An15g01470	AN6611.2	62.m03182	20163.m00245
fphA	Red light phytochrome	An14g02970	AN9008.2	89.m01927	20173.m00405
sakA	MAP kinase represses sexual development	An08g05850	AN1017.2	70.m15235	20180.m01196

Ascomata (Fruit Body) Development

veA	Velvet activator induces sexual reproduction *A.nidulans*	An08g05100	AN1052.2	70.m15191	20173.m00346
nsdD	GATA-transcription factor, light regulation	An02g09610	AN3152.2	59.m08512	20010.m00003
csnD	Signalosome subunit 4, regulation of sexual development	An16g07210	AN1539.2	55.m03058	20171.m00527
csnE	Signalosome subunit 5, regulation of sexual development	An15g06660	AN2129.2	72.m19712	20115.m00100
dopA	Leucine zipper-like domain regulator (initiation morphogenesis)	An11g04750	AN2094.2	57.m05797	20178.m00666
pro1	Cys6-Zn2 transcriptional activator; maturation ascomata	An04g07400[4]	AN1848.2	58.m07662	20129.m00151
pro11	WD40 scaffold protein; regulation fruit body formation	An16g01520	AN8071.2	53.m03924	20167.m00272
mutA	Mutanase, cell wall turnover during sexual development	An06g00510	AN7349.2	57.m05694	20150.m00367
stuA	APSES-transcription factor	An05g00480	AN5836.2	72.m19916	20177.m00377
medA	Transcription factor	An02g02150[2]	AN6230.2	72.m19977	20141.m00193
Nc asd-1	Ascus development; rhamnogalacuronase B	An14g01130	AN7135.2	89.m02015	20153.m00219
Nc asd-4 / areB	Ascus development; GATA-Zn finger transcription factor	An02g02240	AN6221.2	72.m19434	20141.m00163
Pa cro1 (SHE4)	Regulator of myosin; required for syncytial to cellular transition	An18g03150	AN0135.2	71.m15419	20158.m00313
esdC	Required for sexual development in *A. nidulans*	An12g00710	AN9121.2	66.m04577	20169.m00374
ppoA	Fatty acid oxygenase for Psi factor production	An04g05880	AN1967.2	58.m07572	20138.m00158
ppoB	Fatty acid oxygenase for Psi factor production	No definite match	AN6320.2	No definite match	20156.m00214
ppoC	Fatty acid oxygenase for Psi factor production	An02g07930	AN5028.2	59.m09493	20175.m00495
Gz ppoD	Fatty acid oxygenase	An12g01320	No definite match	No definite match	20140.m00151

[1]Gene name derived from *Aspergillus nidulans* where known. Names in parentheses are from *Saccharomyces cerevisiae* . Prefix Nc=*Neurospora crassa* ; Pa=*Podospo*

[2]Partial Sequence found at end/start of contig.

[3]Present in genome but not detected by autoannotation.

[4]Contains internal stop codon.